IN THE CLAIMS

1-32: (cancelled)

33. (new): A method for preventing migration between related host systems or the environment, of a transgene coding for a target protein, the related host systems having cells characterized by cellular compartments, comprising:

(a) obtaining at least a first and a second DNA fragment by splitting a transgene coding for the target protein at one or more predetermined split sites so that the at least first and second DNA fragments code for functionally inactive protein fragments;

(b) introducing the first DNA fragment into a first cellular compartment in the host system and the second DNA fragment into a second cellular compartment for expression therein, wherein the functionally inactive protein fragment encoded by the first DNA fragment is capable of migrating out of the first compartment and being reconstituted with the second functionally inactive protein fragment to form the target protein; and

(c) preventing migration between related host systems or the environment of the transgene coding for the target protein.

34. (new): A method according to claim 33, wherein the first compartment is a mitochondria or a chloroplast.

35. (new): A method according to claim 33, wherein the host system is selected from a plant, an animal or a fungus.

36. (new): A method of claim 33, wherein the at least first and second DNA fragments are each fused to DNA encoding an intein or portion thereof wherein the intein or portion thereof is optionally mutated.

37. (new): A method of claim 36, wherein one of the fusion fragments is formed by linking the 5' end of the DNA fragment coding for an N-terminal portion of the target protein to the 3'-terminal end of the DNA coding for an N-terminal portion of the intein, and another of the fusion fragments is formed by linking the 5'-terminal end of DNA coding for a C-terminal portion of the target protein to the 3'-terminal end of DNA coding for a C-terminal portion of the intein.

38. (new): A method of claim 33, in which the first DNA fragment is fused to a DNA sequence encoding a transit peptide such that the protein products of the DNA fragments are transported into a single compartment where functional reconstitution can occur.

39. (new): A method of claim 33, wherein reconstitution of the target protein from the protein fragments occurs by protein complementation, intein mediated complementation or transplicing.

40. (new): A method of claim 33, wherein the predetermined split site in the transgene corresponds to a split site in a region of the target protein characterized by a non-conserved amino acid sequence.

41. (new): A method of claim 33, wherein the predetermined split site in the transgene corresponds to a region of the target protein characterized by functionally tolerance of linker insertion.

42. (new): A method of claim 33, wherein the predetermined split site in the transgene corresponds to a region of the target protein characterized by a sequence encoding flexible loops.

43. (new): A method of claim 33, wherein the predetermined split site in the transgene corresponds to a region of the target protein characterized by its location between folding domains.

44. (new): A method according to claim 33, wherein the target protein is a protein that induces herbicide resistance in the host system.

45. (new): A method according to claim 44, wherein the target protein is encoded by a mutant acetolactate synthetase gene or a DNA encoding an acetolactactate isoform.

46. (new): A method according to claim 44, wherein the target protein is an ALS protein derived from maize or *E. coli*.

47. (new): A method according to claim 44, wherein the target protein is mutant 5-enolpyruvyl-3-phosphoshikimate synthetase (EPSPS).

48. (new): A method according to claim 44, wherein the herbicide resistance is resistant to glyophosphate.

49. (new): A method of claim 33, wherein the first and second DNA fragments are each fused to DNA coding for one or more affinity domains.

50. (new): A method of claim 49, wherein the affinity domain is selected from the group consisting of inteins or intein fragments, leucine zipper and c-Jun/c-Fos.

51. (new): A method according to claim 33, wherein at least one of the protein fragments is encoded by a DNA selected from SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38 and SEQ ID NO:39.

52. (new): A method according to claim 33, wherein at least one of the protein fragments is encoded by a DNA selected from SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12 and SEQ ID NO:13.

53. (new): A method according to claim 33, wherein at least one of the protein fragments is encoded by a DNA selected from SEQ ID NO:17, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19.

54. (new): A method according to claim 36, wherein the intein is SspDnaE intein or portion thereof wherein the intein is optionally mutated.